results of **BLAST**

Appl.

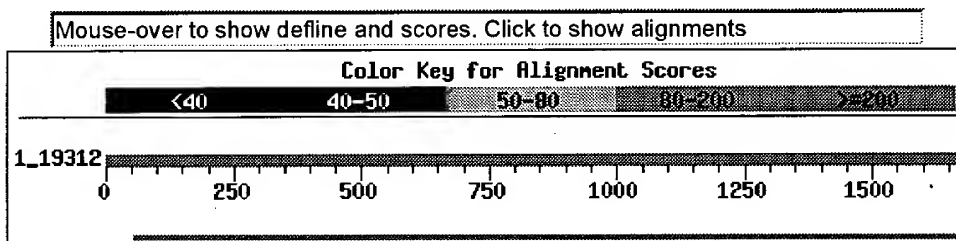
INFO: Entrez query "AF152376" returned no records, with error: NULL returned from EntrezSynchronousQuery()

**BLASTN 2.2.6 [Apr-09-2003]**

RID: 1061432177-19312-234002.BLASTQ3

Query= gi|5870623|gb|AF084467.1|AF084467  
(1669 letters)

Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS,  
GSS, or phase 0, 1 or 2 HTGS sequences)  
1,879,486 sequences; 8,891,580,893 total letters

[Taxonomy reports](#)**Distribution of 2 Blast Hits on the Query Sequence**

Sequences producing significant alignments:	Score (bits)	E Value
gi 5616196 gb AF152376.1 AF152376 Homo sapiens heparanase m...	3126	0.0

**Alignments**

Get selected sequences

Select all

Deselect all

☐ >gi|5616196|gb|AF152376.1|AF152376 Homo sapiens heparanase mRNA, complete cds  
Length = 1694

Score = 3126 bits (1577), Expect = 0.0  
Identities = 1605/1616 (99%), Gaps = 3/1616 (0%)  
Strand = Plus / Plus

Query: 54 cctggggccgctgggtccctctccctggcgccctgccccgacctgcgcaagcacagca 113  
|||||

Sbjct: 65 cctggggccgctgggtccccctctccccctggcgccctgccccgacctgcgcaagcacag-- 122

Query: 114 ggacgtcgtggacctggactttctcaccaggagccgctgcacctggtagccctcggt 173  
 |||

Sbjct: 123 -gacgtcgtggacctggactttctcaccaggagccgctgcacctggtagccctcggt 181

Query: 174 cctgtccgtcaccattgacgccaaacctggccacggaccgcggttcctcatcctcctggg 233  
 |||

Sbjct: 182 cctgtccgtcaccattgacgccaaacctggccacggaccgcggttcctcatcctcctggg 241

Query: 234 ttctccaaagcttcgtaccttggccagaggcttgtctcctgcgtacctgaggtttggtgg 293  
 |||

Sbjct: 242 ttctccaaagcttcgtaccttggccagaggcttgtctcctgcgtacctgaggtttggtgg 301

Query: 294 caccaagacagacttcctaattttcgatcccaagaaggaatcaacctttgaagagagaag 353  
 |||

Sbjct: 302 caccaagacagacttcctaattttcgatcccaagaaggaatcaacctttgaagagagaag 361

Query: 354 ttactggcaatctcaagtcaaccaggatatttgc aaatatggatccatccctcctgatgt 413  
 |||

Sbjct: 362 ttactggcaatctcaagtcaaccaggatatttgc aaatatggatccatccctcctgatgt 421

Query: 414 ggaggagaagttacggttggaatggccctaccaggagcaattgctactccgagaacacta 473  
 |||

Sbjct: 422 ggaggagaagttacggttggaatggccctaccaggagcaattgctactccgagaacacta 481

Query: 474 ccagaaaaagttcaagaacagcacctactcaagaagctctgtagatgtgctatacacttt 533  
 |||

Sbjct: 482 ccagaaaaagttcaagaacagcacctactcaagaagctctgtagatgtgctatacacttt 541

Query: 534 tgcaaaactgctcaggactggacttgatctttggcctaataatgcggttattaagaacagcaga 593  
 |||

Sbjct: 542 tgcaaaactgctcaggactggacttgatctttggcctaataatgcggttattaagaacagcaga 601

Query: 594 tttgcagtggaaacagtttctaatagtcagttgctcctggactactgctcttccaaggggta 653  
 |||

Sbjct: 602 tttgcagtggaaacagtttctaatagtcagttgctcctggactactgctcttccaaggggta 661

Query: 654 taacatttcttggaactaggcaatgaacctaacagtttcccttaagaaggctgatatttt 713  
 |||

Sbjct: 662 taacatttcttggaactaggcaatgaacctaacagtttcccttaagaaggctgatatttt 721

Query: 714 catcaatgggtcgcagttaggagaagattttattcaattgcataaacttctaagaaagtc 773  
 |||

Sbjct: 722 catcaatgggtcgcagttaggagaagattttattcaattgcataaacttctaagaaagtc 781

Query: 774 caccttcaaaaatgcaaaactctatggctcctgatgttggtcagcctcgaagaaagacggc 833  
 |||

Sbjct: 782 caccttcaaaaatgcaaaactctatggctcctgatgttggtcagcctcgaagaaagacggc 841

Query: 834 taagatgctgaagagcttcctgaaggctggtggagaagtgattgattcagttacatggca 893  
|||||  
Sbjct: 842 taagatgctgaagagcttcctgaaggctggtggagaagtgattgattcagttacatggca 901

Query: 894 tcactactatttgaatggacggactgctaccaggggaagattttctaaaccctgatgtatt 953  
|||||  
Sbjct: 902 tcactactatttgaatggacggactgctaccaggggaagattttctaaaccctgatgtatt 961

Query: 954 ggacatttttatttcatctgtgcaaaaagttttccaggtggttgagagcaccaggcctgg 1013  
|||||  
Sbjct: 962 ggacatttttatttcatctgtgcaaaaagttttccaggtggttgagagcaccaggcctgg 1021

Query: 1014 caagaaggtctggttaggagaaacaagctctgcatatggaggcggagcgcccttgctatc 1073  
|||||  
Sbjct: 1022 caagaaggtctggttaggagaaacaagctctgcatatggaggcggagcgcccttgctatc 1081

Query: 1074 cgacacctttgcagctggctttatgtggctggataaattgggcctgtcagcccgaatggg 1133  
|||||  
Sbjct: 1082 cgacacctttgcagctggctttatgtggctggataaattgggcctgtcagcccgaatggg 1141

Query: 1134 aatagaagtggtgatgaggcaagtattctttggagcaggaaactaccatttagtgatga 1193  
|||||  
Sbjct: 1142 aatagaagtggtgatgaggcaagtattctttggagcaggaaactaccatttagtgatga 1201

Query: 1194 aaacttcgatccctttacctgattattggctatctcttctgttcaagaaattggtgggcac 1253  
|||||  
Sbjct: 1202 aaacttcgatccctttacctgattattggctatctcttctgttcaagaaattggtgggcac 1261

Query: 1254 caaggtgttaatggcaagcgtgcaaggttcaaagagaaggaagcttcgagtataccttca 1313  
|||||  
Sbjct: 1262 caaggtgttaatggcaagcgtgcaaggttcaaagagaaggaagcttcgagtataccttca 1321

Query: 1314 ttgcacaaacactgacaatccaaggtataaagaaggagatttaactctgtatgccataaa 1373  
|||||  
Sbjct: 1322 ttgcacaaacactgacaatccaaggtataaagaaggagatttaactctgtatgccataaa 1381

Query: 1374 cctccataacgtcaccaagtaacttgcggttaccctatcctttttctaacaagcaagtggga 1433  
|||||  
Sbjct: 1382 cctccataatgtcaccaagtaacttgcggttaccctatcctttttctaacaagcaagtggga 1441

Query: 1434 taaataccttctaagacctttgggacctcatggattactttccaaatctgtccaactcaa 1493  
|||||  
Sbjct: 1442 taaataccttctaagacctttgggacctcatggattactttccaaatctgtccaactcaa 1501

Query: 1494 tgggtctaactctaaagatggtggatgatcaaacccttgccacctttaatggaaaaacctct 1553  
|||||  
Sbjct: 1502 tgggtctaactctaaagatggtggatgatcaaacccttgccacctttaatggaaaaacctct 1561

Query: 1554 ccggccaggaagttcactgggcttgccagctttctcatatagnnnnnngtgataagaaa 1613  
|||||  
Sbjct: 1562 ccggccaggaagttcactgggcttgccagctttctcatatagtttttttgataagaaa 1621

Query: 1614 tgccaaagttgctgcttgcatctgaaaataaaatatactagtcctgacactgaaaa 1669  
 |||||  
 Sbjct: 1622 tgccaaagttgctgcttgcatctgaaaataaaatatactagtcctgacactgaaaa 1677

Score = 28.2 bits (14), Expect = 0.009  
 Identities = 14/14 (100%)  
 Strand = Plus / Minus

Query: 380 atatttgcaaatat 393  
 |||||  
 Sbjct: 401 atatttgcaaatat 388




Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS,  
 or phase 0, 1 or 2 HTGS sequences)  
 Posted date: Aug 20, 2003 12:00 AM  
 Number of letters in database: -24,009,540  
 Number of sequences in database: 1,779,461

Lambda	K	H
1.37	0.711	1.31

Gapped

Lambda	K	H
1.37	0.711	1.31

Matrix: blastn matrix:1 -3  
 Gap Penalties: Existence: 5, Extension: 2  
 Number of Hits to DB: 0  
 Number of Sequences: 100025  
 Number of extensions: 0  
 Number of successful extensions: 0  
 Number of sequences better than 10.0: 0  
 Number of HSP's better than 10.0 without gapping: 0  
 Number of HSP's successfully gapped in prelim test: 0  
 Number of HSP's that attempted gapping in prelim test: 0  
 Number of HSP's gapped (non-prelim): 0  
 length of query: 3340  
 length of database: 1694  
 effective HSP length: 10  
 effective length of query: 1659  
 effective length of database: 1684  
 effective search space: 2793756  
 effective search space used: 2793756  
 T: 0  
 A: 0  
 X1: 6 (11.9 bits)  
 X2: 15 (29.7 bits)  
 S1: 12 (24.3 bits)  
 S2: 9 (18.3 bits)

